

08/249671

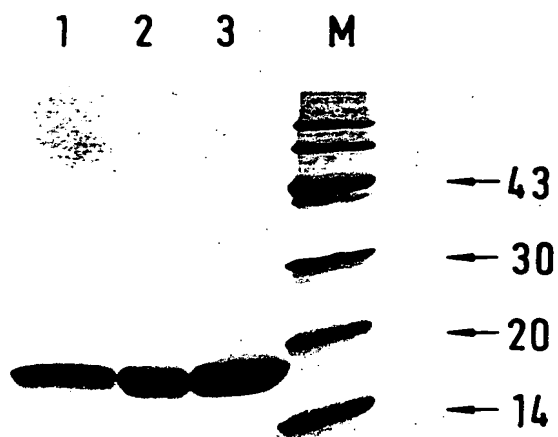
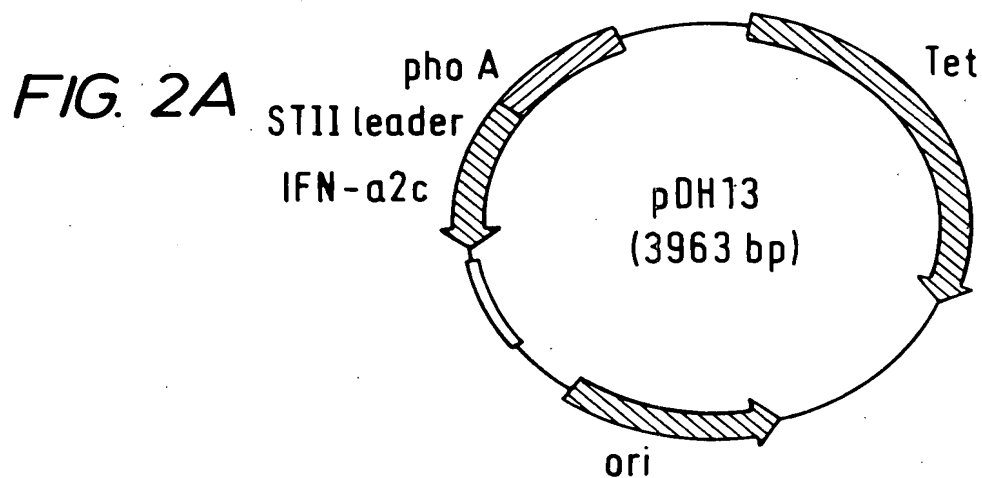
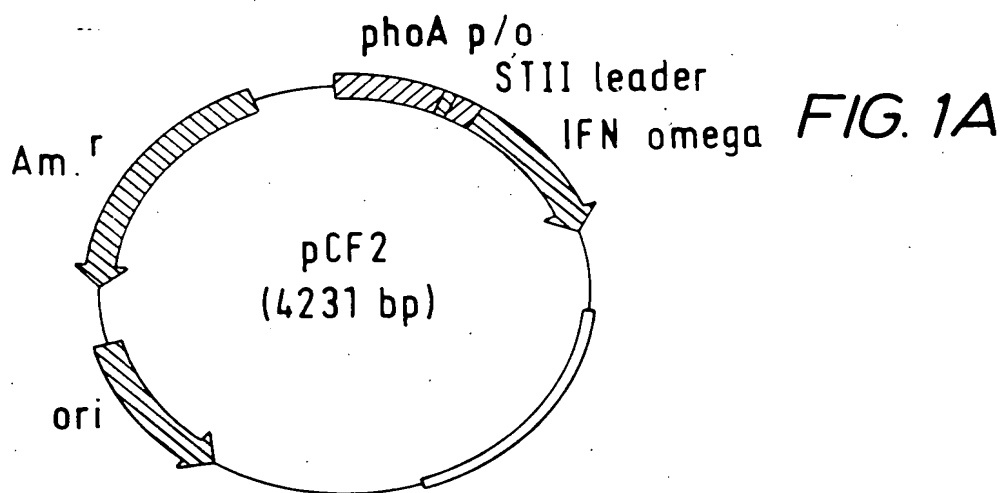


FIG. 4

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FIG. 1B

gaattggagattatcgctcactgcaatgcttcgcaatatggcgcaaaatgaccaac	55
agcggttgattgattcaggtagaggggctgtacgaggtaaagcccgatgccag	110
cattcctgacgacgatacggagctgctgcgcgattacgtaagaagtattgaag	165
catcctcgtcagtaaaaagttaatttttcaacagctgtcataaagtgtcacgg	220
ccgagacttatagtcgctttgttttttttttaattgtattgtcgcgaggttg	275
aggtgatattt ATG AAA AAG AAT ATC GCA TTT CTT CTT GCA TCT	318
M K K N I A F L L A S	11
ATG TTC GTT TTT TCT ATT GCT ACA AAT GCC TAT GCA TGT GAT	360
M F V F S I A T N A Y A C D	25
CTG CCT CAG AAC CAT GGC CTA CTT AGC AGG AAC ACC TTG GTG	402
L P Q N H G L L S R N T L V	39
CTT CTG CAC CAA ATG AGG AGA ATC TCC CCT TTC TTG TGT CTC	444
L L H Q M R I S P F L C L	53
AAG GAC AGA AGA GAC TTC AGG TTC CCC CAG GAG ATG GTA AAA	486
K D R R D F R F P Q E M V K	67
GGG AGC CAG TTG CAG AAG GCC CAT GTC ATG TCT GTC CTC CAT	528
G S Q L Q K A H V M S V L H	81
GAG ATG CTG CAG CAG ATC TTC AGC CTC TTC CAC ACA GAG CGC	570
E M L Q Q I F S L F H T E R	95

FIG. 1B (CONTD)

FIG. 1B (CONTD)

FIG. 2B

ECORI

gaattcgagattatcgctcactgcaatgcttcgcaatatggcgcaaaatgaccaac 55
agcggttgattgatcaggtagaggggctgtacgaggtaaagcccgatgccag 110
cattcctgacgacgatacggagctgctgcggttacgtaaaagaattattgaag 165
catcctcgtagtaaaaagttaattcttttcaacagctgtcataaagttgtcacgg 220

XhoI

ccgagacttatagtcgctttgtttttatttttaattgtattgtcgagaggttg 275

STII Leader peptide ->

aggtgatttt ATG AAA AAG AAT ATC GCA TTT CTT CTT GCA TCT 318
M K K N I A F L L A S 11

IFN α 2c ->

ATG TTC GTT TTT TCT ATT GCT ACA AAT GCC TAT GCA TGT GAT 360
M F V F S I A T N A Y A C D 25
CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG ACC TTG ATG 402
L P Q T H S L G S R R T L M 39
CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC TGC TTG 444
L L A Q M R R I S L F S C L 53
AAG GAC AGA CGT GAC TTT GGA TTT CCC CAG GAG TTT GGC 486
K D R R D F G F P Q E E F G 67

AAC CAG TTC CAA AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG	528
N Q F Q K A E T I P V L H E	81
ATG ATC CAG CAG ATC TTC AAT CTC TTC AGC ACA AAG GAC TCA	570
M I Q Q I F N L F S T K D S	95
TCT GCT GCT TGG GAT GAG ACC CTC CTA GAC AAA TTC TAC ACT	612
S A A W D E T L L D K F Y T	109
GAA CTC TAC CAG CAG CTG AAT GAC CTG GAA GCC TGT GTG ATA	654
E L Y Q Q L N D L E A C V I	123
CAG GGG GTG GGG GTG ACA GAG ACT CCC CTG ATG AAG GAG GAC	696
Q G V G V T E T P L M K E D	137
TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA AGA ATC ACT CTC	738
S I L A V R K Y F Q R I T L	151
TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG GAG GTT	780
Y L K E K K Y S P C A W E V	165
GTC AGA GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC	822
V R A E I M R S F S L S T N	179
PvuI PstI	
TTG CAA GAA AGT TTA AGA AGT AAG GAA tgataacgacgtaactgc	868
L Q E S L R S K E	188
HindIII	
agaagctt	876

FIG. 2B(CONTD)

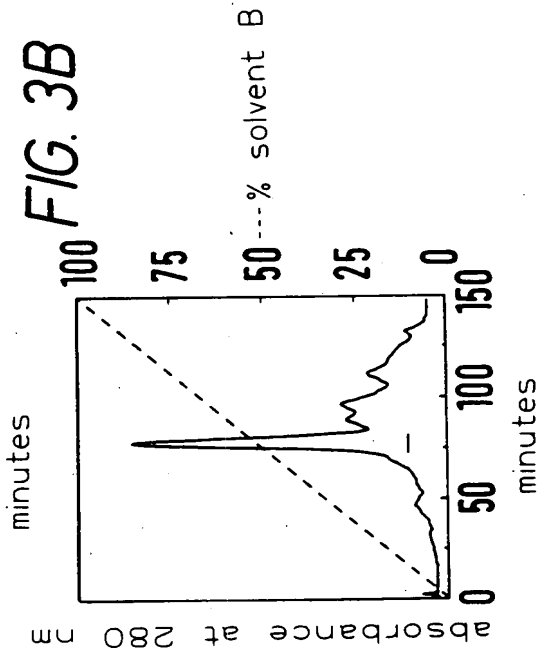
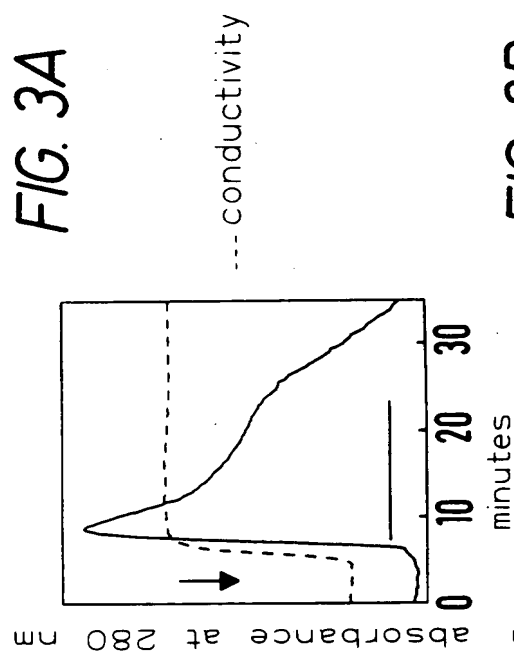
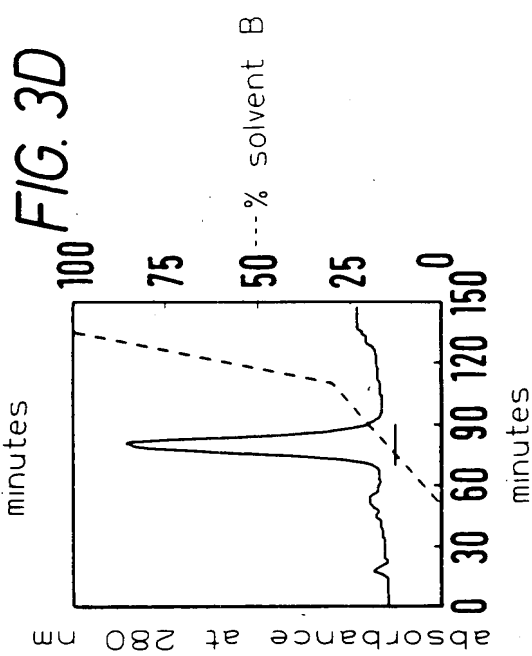
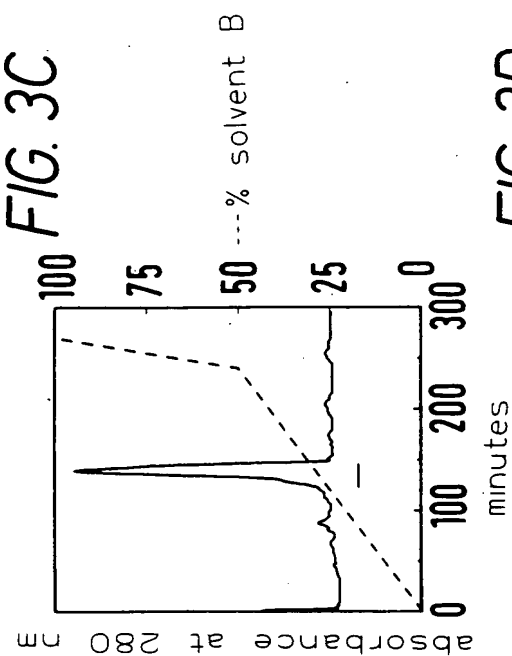


FIG. 5A

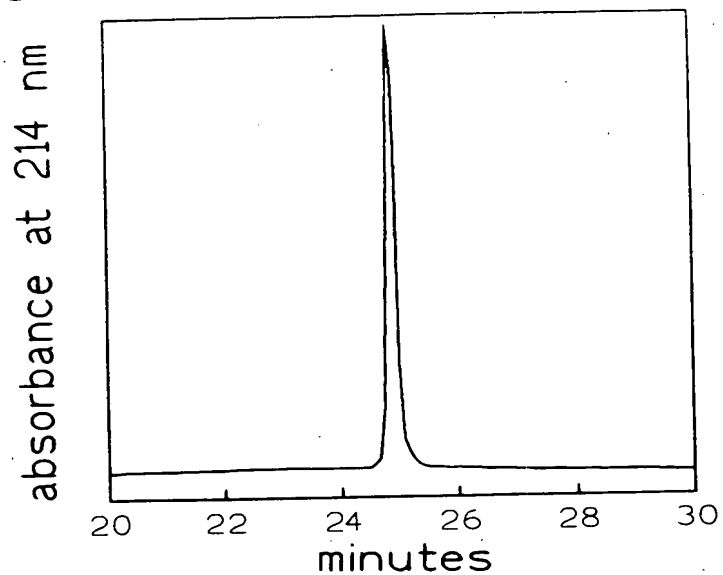
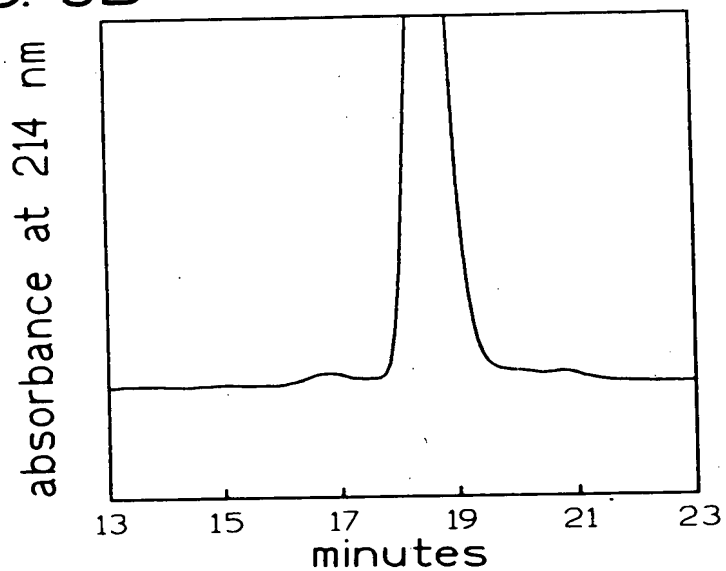


FIG. 5B



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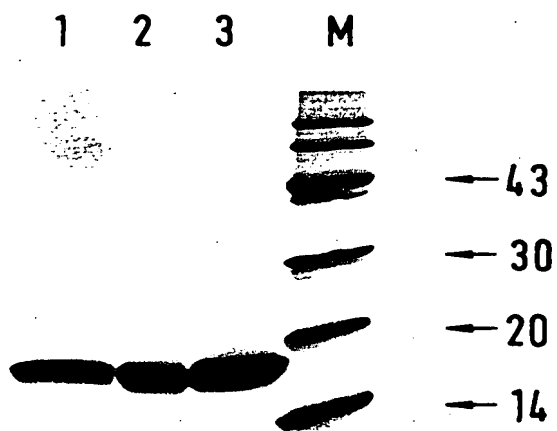
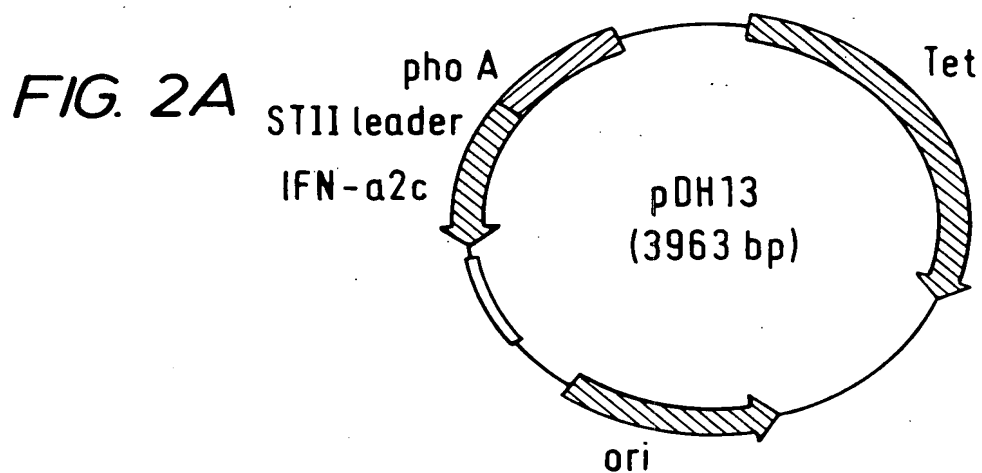
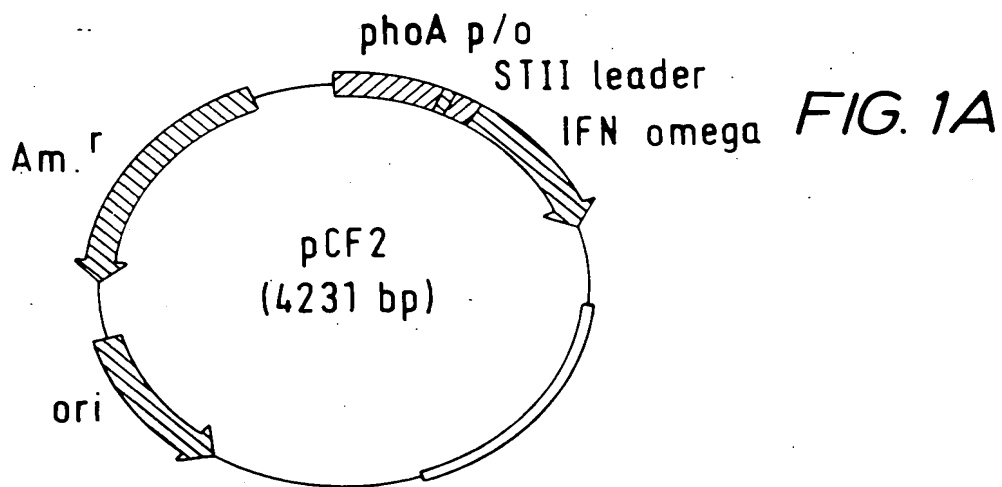


FIG. 4

FIG. 1B

55	gaattggagattatcg	taactgcaatgcttcg	caataatggcg	caaaatgac	caac	
110	agcggttgattgatc	aggtaggggctgtac	gaggtaaagccg	atgccag		
165	cattcctgacgacga	tcgagctgctgcgcg	attacgtaaagaag	tattgaag		
220	catcctcgtcagta	aaaagttaatctttt	caacagctgcataa	agttgtcacgg		
275	ccgagacttatagtc	gcttggttttatttt	taattgattgctcg	agaggttg		
318	aggtgatttt	ATG AAA AAG AAT	ATC GCA TTT	CTT GCA TCT		
11		M K K N I A F L L A S				
360	ATG TTC GTT TTT	TCT ATT GCT ACA	AAT GCC TAT	GCA TGT GAT		
25	M F V F S I A T N A Y A C D					
402	CTG CCT CAG AAC	CAT GGC CTA CTT	AGC AGG AAC	ACC TTG GTG		
39	L P Q N H G L L S R N T L V					
444	CTT CTG CAC CAA	ATG AGG AGA ATC	TCC CCT TTC	TTG TGT CTC		
53	L L H Q M R R I S P F L C L					
486	AAG GAC AGA AGA	GAC TTC AGG TTC	CCC CAG GAG	ATG GTA AAA		
67	K D R R D F R F P Q E M V K					
528	GGG AGC CAG TTG	CAG AAG GCC CAT	GTC ATG TCT	GTC CTC CAT		
81	G S Q L Q Q K A H V M S V L H					
570	GAG ATG CTG CAG	CAG ATC TTC	AGC CTC TTC	CAC ACA GAG	CGC	
95	E M L Q Q Q I F S L F H T E R					

FIG. 1B (CONT'D)

FIG. 2B

ECORI

gaattcgagattatcgtcactgcaatgcttcgcaatatggcgcaaaatgaccaac 55
agcggttgattgatcaggtagagggggtgctgtacgaggtaaagcccgatgccag 110
cattcctgacgacgatacggagctgctgctgattacgtaaaagaattattgaag 165
catcctcgtaaaaaagtttaattcttttcaacagctgtcataaagtgtcacgg 220

XhoI

ccgagacttatagtcgcttggttttttatttttttaattgttctcgagaggttg 275

STII Leader peptide ->

aggtgatttt ATG AAA AAG AAT ATC GCA TTT CTT CTT GCA TCT 318
M K K N I A F L L A S 11

IFNa2c ->

ATG TTC GTT TTT TCT ATT GCT ACA AAT GCC TAT GCA TGT GAT 360
M F V F S I A T N A Y A C D 25
CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG ACC TTG ATG 402
L P Q T H S L G S R R T L M 39
CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC TGC TTG 444
L L A Q M R R I S L F S C L 53
AAG GAC AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC 486
K D R R D F G G F P O E E F G 67

AAC CAG TTC CAA AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG	528
N Q F Q K A E T I P V L H E	81
ATG ATC CAG CAG ATC TTC AAT CTC TTC AGC ACA AAG GAC TCA	570
M I Q Q I F N L F S T K D S	95
TCT GCT GCT TGG GAT GAG ACC CTC CTA GAC AAA TTC TAC ACT	612
S A A W D E T L L D K F Y T	109
GAA CTC TAC CAG CAG CTG AAT GAC CTG GAA GCC TGT GTG ATA	654
E L Y Q Q L N D L E A C V I	123
CAG GGG GTG GGG GTG ACA GAG ACT CCC CTG ATG AAG GAG GAC	696
Q G V G V T E T P L M K E D	137
TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA AGA ATC ACT CTC	738
S I L A V R K Y F Q R I T L	151
TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG GAG GTT	780
Y L K E K K Y S P C A W E V	165
GTC AGA GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC	822
V R A E I M R S S F S L S T N	179
	PvuI PstI
TTG CAA GAA AGT TTA AGA AGT AAG GAA tgataacgacgtaactgc	868
L Q E S L R S K E	188
HindIII	
agaagctt	876

FIG. 2B (CONT'D)

